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Search Results -

Terms	Documents
L7 not radio	6

Database: US Patents Full-Text Database
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JPO Abstracts Database
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IBM Technical Disclosure Bulletins

Search: L8

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DATE: Thursday, October 16, 2003 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT; PLUR=YES; OP=OR			
L8	L7 not radio	6	L8
L7	l5 not radioactive	13	L7
L6	L5 same (advantag$ or useful$)	1	L6
L5	L3 same (bromine or iodine)	28	L5
L4	L3 same defect	6	L4
L3	L1 same mass same label$	3640	L3
L2	L1 same (mass near0 defect)	0	L2
L1	oligomer or oligonucleotide or polynucleotide or DNA or RNA or protein or lipid	192712	L1

END OF SEARCH HISTORY

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Search Results -

Terms	Documents
L2 same label$ same fragment	7

Database: US Patents Full-Text Database
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Derwent World Patents Index
IBM Technical Disclosure Bulletins

Search: L6

Refine Search

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Search History

DATE: Thursday, October 16, 2003 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT; PLUR=YES; OP=OR			
L6	L2 same label$ same fragment	7	L6
L5	L2 same label$ same oligomer	0	L5
L4	L2 same label$ oligomer	45788	L4
L3	L2 same (label$ near0 oligomer)	0	L3
L2	L1 same identif$	1075	L2
L1	mass near0 spectrum	13100	L1

END OF SEARCH HISTORY

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FILE 'BIOSIS' ENTERED AT 16:07:48 ON 16 OCT 2003
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FILE 'CAPLUS' ENTERED AT 16:07:48 ON 16 OCT 2003
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=> s mass(wdefect
MISSING OPERATOR 'MASS(WDEFECT'
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s mass(w)defect
L1          378 MASS(W) DEFECT

=> s l1(p)label?
L2            3 L1(P) LABEL?

=> d bib ab l2 1-3

L2   ANSWER 1 OF 3  CAPLUS  COPYRIGHT 2003 ACS on STN
AN   2002:658346  CAPLUS
DN   137:165811
TI   Mass defect labeling for the determination
     of oligomer sequences
IN   Schneider, Luke V.; Hall, Michael P.; Petesch, Robert
PA   Target Discovery, Inc, USA
SO   PCT Int. Appl., 123 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 2
     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
     ---------------   ----  --------       ---------------  --------
PI   WO 2002066952     A2    20020829       WO 2001-US49951  20011019
     WO 2002066952     A3    20030904
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL,
             PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG,
             US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
             DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
             BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
     US 2002172961     A1    20021121       US 2001-35349    20011019
PRAI US 2000-242165P   P     20001019
     US 2000-242398P   P     20001019
AB   The invention concerns mass tagging methods are provided that lead to mass
     spectrometer detection sensitivities and mol. discriminations that are
     improved over other methods.  In particular the methods are useful for
     discriminating tagged mols. and fragments of mols. from chem. noise in the
     mass spectrum.  These mass tagging methods are useful for oligomer
     sequencing, detg. the relative abundances of mols. from different samples,
     and identifying individual mols. or chem. processing steps in
     combinatorial chem. libraries.  The methods provided are useful for the
     simultaneous anal. of multiple mols. and reaction mixts. by mass
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spectrometric methods.

L2 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2002:595153 CAPLUS
DN 137:152020
TI Mass spectrometric methods for determining terminal oligomer sequences in proteins and nucleic acids and oligosaccharides and lipids
IN Schneider, Luke V.; Petesch, Robert; Hall, Michael P.
PA Target Discovery, Inc., USA
SO PCT Int. Appl., 151 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002061661	A2	20020808	WO 2001-US49491	20011019
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	US 2002172961	A1	20021121	US 2001-35349	20011019
PRAI	US 2000-242165P	P	20001019		
	US 2000-242398P	P	20001019		

AB Methods and app. are provided for deriving the sequence of an oligomer, and in particular a terminal portion of an oligomer **labeled** with a **mass defect label**. A math. algorithm is provided for detg. a protein sequence tag directly from mass spectra of fragmented **labeled** proteins. The algorithm requires the use of both the mass-to-charge position of a signal and its relative abundance, and further consists of a cumulative sequence ranking system in which the relative abundance of the ions predicted to result from each possible sequence are combined by product or summation with the relative abundances of ions predicted to result from subsequent residues. Thus, in one exemplary method for deriving the sequence of a polypeptide, a predetd. set of mass/charge values for amino acid sequences is stored. An abundance value from mass spectrum data for each mass/charge value in the predetd. set is detd. to produce a plurality of abundance values. A first ranking, based on the plurality of abundance values, is calcd. for each sequence of a set of amino acid sequences having a first no. of amino acids. A second ranking, based on the plurality of abundance values, for each sequence of a set of amino acid sequences having a second no. of amino acids is calcd. A cumulative ranking, based on the first ranking and the second ranking, is calcd. for each sequence of a set of amino acid sequences having at least the second no. of amino acids. The method is also exemplified for the sequence anal. of nucleic acids and oligosaccharides, and for identification of fatty acid compn. and arrangement in lipids (lipid sequencing). A no. of photocleavable **mass defect labels** are described.

L2 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1980:31407 CAPLUS
DN 92:31407
TI Rearrangement of a vibrational spectrum of a crystal in the presence of impurity states of a large radius
AU Ivanov, M. A.; Pogorelov, Yu. G.
CS Inst. Metallofiz., Kiev, USSR
SO Fizika Nizkikh Temperatur (Kiev) (1979), 5(8), 910-24

CODEN: FNTEDK; ISSN: 0132-6414
DT Journal
LA Russian
AB The phonon spectrum of a crystal contg. impurities is considered, both the **mass defect** and the change in force consts. being taken into account. In the system contg. long range impurity states a small characteristic concn. of impurities exists at which the spectrum is essentially redistributed near the impurity mode frequency. Two kinds of possible rearrangement (coherent and incoherent) are found. For low-frequency quasilocal vibrations the rearrangement (coherent and incoherent) are found. For low-frequency quasilocal vibrations the rearrangement is always coherent and the spectrum is cross splitted. When the impurity level is close to the optical band edge (or to the top of the acoustic band) both types of rearrangement can occur depending on the relation between the perturbation parameters. With low impurity concns., a new (impurity) band where the states are crystal momentum **labeled** could appear provided that the impurities are weakly bound and light. An influence of the coherent rearrangement on the character of the optical spectra of impurity states is discussed.

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FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE' ENTERED AT 16:07:48 ON 16 OCT 2003
L1 378 S MASS(W)DEFECT
L2 3 S L1(P)LABEL?